

#6

OIPE

RAW SEQUENCE LISTING

DATE: 08/21/2001

PATENT APPLICATION: US/09/800,103

TIME: 11:49:41

Input Set : A:\LEX-0143-USA SEQLIST.txt

Output Set: N:\CRF3\08162001\I800103.raw

ENTERED

4 <110> APPLICANT: Donoho, Gregory
 5 Scoville, John
 6 Zambrowicz, Brian
 7 Cullinan, Emily
 8 Kieke, James A.
 9 Hu, Yi
 10 Turner, C. Alexander Jr.
 11 Walke, D. Wade
 13 <120> TITLE OF INVENTION: Novel Human Transporter Proteins and
 14 Polynucleotides Encoding the Same
 17 <130> FILE REFERENCE: Lex-0143-USA
 19 <140> CURRENT APPLICATION NUMBER: US/09/800,103
 19 <141> CURRENT FILING DATE: 2001-03-06
 19 <150> PRIOR APPLICATION NUMBER: US 60/187,120
 20 <151> PRIOR FILING DATE: 2000-03-06
 22 <150> PRIOR APPLICATION NUMBER: US 60/204,725
 23 <151> PRIOR FILING DATE: 2000-05-16
 25 <160> NUMBER OF SEQ ID NOS: 40
 27 <170> SOFTWARE: FastSEQ for Windows Version 4.0
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 30 <211> LENGTH: 1311
 31 <212> TYPE: DNA
 32 <213> ORGANISM: Homo sapiens
 34 <400> SEQUENCE: 1
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 36 cccgagtgcc aggcattggac ggggacgctg ctgctgggca cgtgccttct gtactgcgcc 120
 37 cgctccagca tgcccatctg caccgtctcc atgagccagg acttcggctg gaacaagaag 180
 38 gaggcgggca tcgtgctcag cagcttcttc tggggctact gcctgacaca ggttggtggc 240
 39 ggccacctcg gggatcggat tgggggtgag aaggtcatcc tgctgtcagc ctctgcctgg 300
 40 ggctccatca cggccgtcac cccactgctc gccacactga gcagtgccca cctggccttc 360
 41 atgaccttct cagcctacct catgggcttg ctccaagggg tttacttccc tgccctgacc 420
 42 agcctgctgt cgcagaaggc gcgggagagt gagecagcct tcacctacag catcgtgggc 480
 43 gccggtctcc agtttgggac gctgctgacc ggggcgggtg gctccctgct cctggaatgg 540
 44 tacggttggc agagcattct ctatttctcc ggcggcctca ccttgctttg ggtgtggtac 600
 45 gtgtacaggt acctgctgag tgaaaaagat ctcatccttg ccttggtgtg cctggcccaa 660
 46 agccggccgg tgtccaggca cagcagagtc cctggagac ggctcttccg gaagcctgct 720
 47 gtctgggcag ccgtcgtctc ccagctctct gcagcctgct ccttcttcat cctcctctcc 780
 48 tggctgcccc ccttcttcga ggagacctc cccgacgcca agggctggat cttcaacgtg 840
 49 gttccttggt tgggtggcat tccggccagt ctattcagcg ggtttctctc tgatcatctc 900
 50 atcaatcagg gttacagac catcacggtg cggaagctca tgcagggcat gggccttggc 960
 51 ctctccagcg tctttgctct gtgcttgggc cacacctcca gcttctgtga gtctgtggtc 1020
 52 tttgcatcag cctccatcgg cctccagacc ttcaaccaca gtggcatttc tgttaacatc 1080
 53 caggacttgg ccccgctcctg cgccggcttt ctggttggtg tggccaacac agccgggggc 1140
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 55 acttgctgt tcaaccttgt ggccatcatc agcaacctgg ggctgtgcac cttcctggtg 1260
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 58 <210> SEQ ID NO: 2

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59 <211> LENGTH: 436
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66 Gln Trp Ser Arg Pro Glu Cys Gln Ala Trp Thr Gly Thr Leu Leu Leu
67 20 25 30
68 Gly Thr Cys Leu Leu Tyr Cys Ala Arg Ser Ser Met Pro Ile, Cys Thr
69 35 40 45
70 Val Ser Met Ser Gln Asp Phe Gly Trp Asn Lys Lys Glu Ala Gly Ile
71 50 55 60
72 Val Leu Ser Ser Phe Phe Trp Gly Tyr Cys Leu Thr Gln Val Val Gly
73 65 70 75 80
74 Gly His Leu Gly Asp Arg Ile Gly Gly Glu Lys Val Ile Leu Leu Ser
75 85 90 95
76 Ala Ser Ala Trp Gly Ser Ile Thr Ala Val Thr Pro Leu Leu Ala His
77 100 105 110
78 Leu Ser Ser Ala His Leu Ala Phe Met Thr Phe Ser Arg Ile Leu Met
79 115 120 125
80 Gly Leu Leu Gln Gly Val Tyr Phe Pro Ala Leu Thr Ser Leu Leu Ser
81 130 135 140
82 Gln Lys Val Arg Glu Ser Glu Arg Ala Phe Thr Tyr Ser Ile Val Gly
83 145 150 155 160
84 Ala Gly Ser Gln Phe Gly Thr Leu Leu Thr Gly Ala Val Gly Ser Leu
85 165 170 175
86 Leu Leu Glu Trp Tyr Gly Trp Gln Ser Ile Phe Tyr Phe Ser Gly Gly
87 180 185 190
88 Leu Thr Leu Leu Trp Val Trp Tyr Val Tyr Arg Tyr Leu Leu Ser Glu
89 195 200 205
90 Lys Asp Leu Ile Leu Ala Leu Gly Val Leu Ala Gln Ser Arg Pro Val
91 210 215 220
92 Ser Arg His Ser Arg Val Pro Trp Arg Arg Leu Phe Arg Lys Pro Ala
93 225 230 235 240
94 Val Trp Ala Ala Val Val Ser Gln Leu Ser Ala Ala Cys Ser Phe Phe
95 245 250 255
96 Ile Leu Leu Ser Trp Leu Pro Thr Phe Phe Glu Glu Thr Phe Pro Asp
97 260 265 270
98 Ala Lys Gly Trp Ile Phe Asn Val Val Pro Trp Leu Val Ala Ile Pro
99 275 280 285
100 Ala Ser Leu Phe Ser Gly Phe Leu Ser Asp His Leu Ile Asn Gln Gly
101 290 295 300
102 Tyr Arg Ala Ile Thr Val Arg Lys Leu Met Gln Gly Met Gly Leu Gly
103 305 310 315 320
104 Leu Ser Ser Val Phe Ala Leu Cys Leu Gly His Thr Ser Ser Phe Cys
105 325 330 335
106 Glu Ser Val Val Phe Ala Ser Ala Ser Ile Gly Leu Gln Thr Phe Asn
107 340 345 350
108 His Ser Gly Ile Ser Val Asn Ile Gln Asp Leu Ala Pro Ser Cys Ala

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109          355          360          365
110 Gly Phe Leu Phe Gly Val Ala Asn Thr Ala Gly Ala Leu Ala Gly Val
111          370          375          380
112 Val Gly Val Cys Leu Gly Gly Tyr Leu Met Glu Thr Thr Gly Ser Trp
113 385          390          395          400
114 Thr Cys Leu Phe Asn Leu Val Ala Ile Ile Ser Asn Leu Gly Leu Cys
115          405          410          415
116 Thr Phe Leu Val Phe Gly Gln Ala Gln Arg Val Asp Leu Ser Ser Thr
117          420          425          430
118 His Glu Asp Leu
119          435
121 <210> SEQ ID NO: 3
122 <211> LENGTH: 1179
123 <212> TYPE: DNA
124 <213> ORGANISM: Homo sapiens
126 <400> SEQUENCE: 3
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128 acggggacgc tgcgtctggg cacgtgcctt ctgtactgcg cccgctccag catgcccata      120
129 tgcaccgtct ccatgagcca ggaacttcggc tggacaaga aggaggccgg catcgtgctc      180
130 agcagcttct tctggggcta ctgctgaca caggttgtgg gcggccacct cggggatcgg      240
131 attgggggtg agaaggtcat cctgctgtca gcctctgcct ggggctccat cacggccgtc      300
132 accccactgc tgcgccacct gagcagtgcc cacctggcct tcatgacctt ctcacgcata      360
133 ctcatgggct tgcctcaagg ggtttacttc cctgcccaga ccagcctgct gtcgcagaag      420
134 gtgcgggaga gtgagcgagc cttaacctac agcatcgtgg gcgcccggct ccagtttggg      480
135 acgctgctga ccggggcggt gggctcccctg ctccctggaat ggtacggctg gcagagcata      540
136 ttctatttct ccggcgccct caccttgctt tgggtgtggt acgtgtacag gtacctgctg      600
137 agtgaaaaag atctcatcct ggccttgggt gtccctggccc aaagccggcc ggtgtccagg      660
138 cacagcagag tcccctggag acggctcttc cgggaagcctg ctgtctgggc agccgtcgtc      720
139 tcccagctct ctgcagcctg ctccctcttc atccctctct cctggctgcc cacctctctc      780
140 gaggagacct tcccgcagcg caagggtctg atcttcaacg tggttccttg gttggtggcg      840
141 attccggcca gtctattcag cgggtttctc tctgatcacc tcatcaatca gggttacaga      900
142 gccatcacgg tgcggaagct catgcagggc atgggccttg gcctctccag cgtctttgct      960
143 ctgtgcctgg gccacacctc cagcttctgt gagtctgtgg tctttgcata agcctccata      1020
144 ggccctccaga ctttcaacca cagtggcatt tctgttaaca tccaggactt ggccccgtcc      1080
145 tgcgcgggct ttctgtttgg tgtggccaac acagccgggg ccttggcagg tgagggggcg      1140
146 gcctctgtgc ccaggagttc ccctgtctgt ggggtttga      1179
148 <210> SEQ ID NO: 4
149 <211> LENGTH: 392
150 <212> TYPE: PRT
151 <213> ORGANISM: Homo sapiens
153 <400> SEQUENCE: 4
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155 1          5          10          15
156 Cys Gln Ala Trp Thr Gly Thr Leu Leu Gly Thr Cys Leu Leu Tyr
157          20          25          30
158 Cys Ala Arg Ser Ser Met Pro Ile Cys Thr Val Ser Met Ser Gln Asp
159          35          40          45
160 Phe Gly Trp Asn Lys Lys Glu Ala Gly Ile Val Leu Ser Ser Phe Phe
161          50          55          60

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162 Trp Gly Tyr Cys Leu Thr Gln Val Val Gly Gly His Leu Gly Asp Arg
163 65 70 75 80
164 Ile Gly Gly Glu Lys Val Ile Leu Leu Ser Ala Ser Ala Trp Gly Ser
165 85 90 95
166 Ile Thr Ala Val Thr Pro Leu Leu Ala His Leu Ser Ser Ala His Leu
167 100 105 110
168 Ala Phe Met Thr Phe Ser Arg Ile Leu Met Gly Leu Leu Gln Gly Val
169 115 120 125
170 Tyr Phe Pro Ala Leu Thr Ser Leu Leu Ser Gln Lys Val Arg Glu Ser
171 130 135 140
172 Glu Arg Ala Phe Thr Tyr Ser Ile Val Gly Ala Gly Ser Gln Phe Gly
173 145 150 155 160
174 Thr Leu Leu Thr Gly Ala Val Gly Ser Leu Leu Leu Glu Trp Tyr Gly
175 165 170 175
176 Trp Gln Ser Ile Phe Tyr Phe Ser Gly Gly Leu Thr Leu Leu Trp Val
177 180 185 190
178 Trp Tyr Val Tyr Arg Tyr Leu Leu Ser Glu Lys Asp Leu Ile Leu Ala
179 195 200 205
180 Leu Gly Val Leu Ala Gln Ser Arg Pro Val Ser Arg His Ser Arg Val
181 210 215 220
182 Pro Trp Arg Arg Leu Phe Arg Lys Pro Ala Val Trp Ala Ala Val Val
183 225 230 235 240
184 Ser Gln Leu Ser Ala Ala Cys Ser Phe Phe Ile Leu Leu Ser Trp Leu
185 245 250 255
186 Pro Thr Phe Phe Glu Glu Thr Phe Pro Asp Ala Lys Gly Trp Ile Phe
187 260 265 270
188 Asn Val Val Pro Trp Leu Val Ala Ile Pro Ala Ser Leu Phe Ser Gly
189 275 280 285
190 Phe Leu Ser Asp His Leu Ile Asn Gln Gly Tyr Arg Ala Ile Thr Val
191 290 295 300
192 Arg Lys Leu Met Gln Gly Met Gly Leu Gly Leu Ser Ser Val Phe Ala
193 305 310 315 320
194 Leu Cys Leu Gly His Thr Ser Ser Phe Cys Glu Ser Val Val Phe Ala
195 325 330 335
196 Ser Ala Ser Ile Gly Leu Gln Thr Phe Asn His Ser Gly Ile Ser Val
197 340 345 350
198 Asn Ile Gln Asp Leu Ala Pro Ser Cys Ala Gly Phe Leu Phe Gly Val
199 355 360 365
200 Ala Asn Thr Ala Gly Ala Leu Ala Gly Glu Gly Arg Ala Ser Val Pro
201 370 375 380
202 Arg Ser Ser Pro Val Cys Gly Val
203 385 390
205 <210> SEQ ID NO: 5
206 <211> LENGTH: 1197
207 <212> TYPE: DNA
208 <213> ORGANISM: Homo sapiens
210 <400> SEQUENCE: 5
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212 cccgagtgcc aggcattggac ggggacgctg ctgctgggca cgtgccttct gtactgcgcc 120

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213 cgctccagca tgcccatctg caccgtctcc atgagccagg acttcgggtg gaacaagaag 180
214 gaggccggca tcgtgctcag cagcttcttc tggggctact gcctgacaca ggttggtggc 240
215 ggccacctcg gggatcggat tgggggtgag aaggtcatcc tgctgtcagc ctctgcctgg 300
216 ggctccatca cggcgcgcac cccactgctc gccacactga gcagtgccca cctggccttc 360
217 atgaccttct cagcatcct catgggcttg ctccaagggg ttacttccc tgccctgacc 420
218 agcctgctgt cgcagaaggt gcgggagagt gagcgagcct tcacctacag catcgtgggc 480
219 gccggctccc agtttgggac gctgctgacc ggggcggtgg gctccctgct cctggaatgg 540
220 tacggctggc agagcatctt ctatttctcc ggcggcctca ccttgctttg ggtgtggtac 600
221 gtgtacaggt acctgctgag tgaaaaagat ctcatcctgg ccttggggtg cctggcccaa 660
222 agccggccgg tgtccaggca cagcagagtc ccctggagac ggctcttccg gaagcctgct 720
223 gtctgggag cgcgtgctc ccagctctct gcagcctgct ccttcttcat cctcctctcc 780
224 tggtgcccc ccttcttcca ggagaccttc cccgacgcca agggctggat ctccaacgtg 840
225 gttccttggg tgggtggcag tccggccagt ctattcagcg ggttctctc tgatcatctc 900
226 atcaatcagg gttacagagc catcacggtg cggaaagctca tgcagggcat gggccttggc 960
227 ctctccagcg tcttctctct gtgcctgggc cacacctcca gcttctgtga gctgtggtc 1020
228 ttgcatcag cctccatcgg cctccagacc ttcaaccaca gtggcatttc tgttaacatc 1080
229 caggacttgg ccccgctcgt cgcgggcttt ctgtttgggtg tggccaacac agccggggcc 1140
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232 <210> SEQ ID NO: 6

233 <211> LENGTH: 398

234 <212> TYPE: PRT

235 <213> ORGANISM: Homo sapiens

237 <400> SEQUENCE: 6

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241 20 25 30
242 Gly Thr Cys Leu Leu Tyr Cys Ala Arg Ser Ser Met Pro Ile Cys Thr
243 35 40 45
244 Val Ser Met Ser Gln Asp Phe Gly Trp Asn Lys Lys Glu Ala Gly Ile
245 50 55 60
246 Val Leu Ser Ser Phe Phe Trp Gly Tyr Cys Leu Thr Gln Val Val Gly
247 65 70 75 80
248 Gly His Leu Gly Asp Arg Ile Gly Gly Glu Lys Val Ile Leu Leu Ser
249 85 90 95
250 Ala Ser Ala Trp Gly Ser Ile Thr Ala Val Thr Pro Leu Leu Ala His
251 100 105 110
252 Leu Ser Ser Ala His Leu Ala Phe Met Thr Phe Ser Arg Ile Leu Met
253 115 120 125
254 Gly Leu Leu Gln Gly Val Tyr Phe Pro Ala Leu Thr Ser Leu Leu Ser
255 130 135 140
256 Gln Lys Val Arg Glu Ser Glu Arg Ala Phe Thr Tyr Ser Ile Val Gly
257 145 150 155 160
258 Ala Gly Ser Gln Phe Gly Thr Leu Leu Thr Gly Ala Val Gly Ser Leu
259 165 170 175
260 Leu Leu Glu Trp Tyr Gly Trp Gln Ser Ile Phe Tyr Phe Ser Gly Gly
261 180 185 190
262 Leu Thr Leu Leu Trp Val Trp Tyr Val Tyr Arg Tyr Leu Leu Ser Glu
263 195 200 205

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/800,103

DATE: 08/21/2001

TIME: 11:49:42

Input Set : A:\LEX-0143-USA SEQLIST.txt

Output Set: N:\CRF3\08162001\I800103.raw

L:19 M:270 C: Current Application Number differs, Replaced Current Application No

L:19 M:271 C: Current Filing Date differs, Replaced Current Filing Date